

16C/ 1635

OIE

7 / K.T.
1/25

RAW SEQUENCE LISTING

DATE: 01/03/2002

PATENT APPLICATION: US/09/671,687A

TIME: 14:55:14

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\01032002\I671687A.raw

Raw
Seq
Listing

ENTERED

RECEIVED

JAN 24 2001

TECH CENTER 1600/2900

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3 <110> APPLICANT: WALLACH, David
4      KOVALENKO, Andrei
5      CANTARELLA, Giuseppina
7 <120> TITLE OF INVENTION: INHIBITOR OF NF-kB ACTIVATOR
9 <130> FILE REFERENCE: WALLACH=25
11 <140> CURRENT APPLICATION NUMBER: 09/671,687A
12 <141> CURRENT FILING DATE: 2000-09-28
14 <150> PRIOR APPLICATION NUMBER: 09/646,403
15 <151> PRIOR FILING DATE: 2000-09-18
17 <150> PRIOR APPLICATION NUMBER: IL 126024
18 <151> PRIOR FILING DATE: 1998-09-01
20 <150> PRIOR APPLICATION NUMBER: IL 134604
21 <151> PRIOR FILING DATE: 2000-02-17
23 <160> NUMBER OF SEQ ID NOS: 4
25 <170> SOFTWARE: PatentIn version 3.1
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65 cactgaccac cgagaacaga ttccactctt taccattcag tctcaccaag atgcccata      120
67 ccaatggaag tattggccac agtccacttt ctctgtcagc ccagtctgta atggaagagc      180
69 taaacactgc acccgtccaa gagagtccac ccttggccat gcctcctggg aactcacatg      240
71 gtctagaagt gggctcattg gctgaagtta aggagaaccc tcctttctat ggggtaatcc      300
73 gttggatcgg tcagccacca ggactgaatg aagtgtctgc tggactggaa ctggaagatg      360
75 agtgtgcagg ctgtacggat ggaaccttca gaggcactcg gtatttcacc tgtgcctga      420

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77 agaaggcgct gtttgtgaaa ctgaagagct gcaggcctga ctctagggtt gcatcattgc 480
79 agccgggttt caatcaagat tgagcgctgt aactctttag catttgagg ctacttaagt 540
W--> 81 gaagtagtng aagaaaatac tnccanccaa aaatggaaaa agaargcttg gagataatga 600
W--> 83 ttgggggaaag aagaaaggca tccaagggtc attacaattc ttgktactta gnactcaacc 660
85 ttattctkgc ttatttkgct tttagttctg ttctnnggaca ctggtgttac tttagacccc 720
87 aaagaaaaag aaacgatgtt agaataattwt wkwgmmaccc aagagctact gaggacagaa 780
89 attgttaatc ctctgagaat atatggatat gtgtgtgccca caaaaattat gaaactgagg 840
91 aaaatacttg aaaagggtga ggctgcatca ggatttacct ctgaagaaaa agatcctgag 900
93 gaattcttga atattctgtt tcatcatatt ttaagggtag aacctttgct aaaaaataaga 960
95 tcagcaggtc aaaaggtaaa agattgttac ttctatcaaa tttttatgga aaaaaatgag 1020
97 aaagttggcg ttcccacaat tcagcagttg ttagaatggt cttttatcaa cagtaacctg 1080
99 aaatttgagc aggcaccatc atgtctgatt attcagatgc ctcgatttgg aaaagacttt 1140
101 aaactattta aaaaattttt cttctctggt aattagatat aacagattta cttgaagaca 1200
103 cccagacag tgccggatat gtggagggtc tgcaatgtat gagtgtaga atgctacgac 1260
105 gatccggaca ccagctggaa aaacaagcag ttttgtaaaa cctgcaacac tcaagtccac 1320
107 cttcatccga agaggctgaa tcataaatat aaccagtggt cacttcccaa agacttacc 1380
109 cgactgggag attggagaca cggctgcatc ccttgccaga atatggagt atttgctgtt 1440
111 ctctgcatag aaacaagcca ctatgttgct tttgtgaagt atgggaagga cgattctgcc 1500
113 tggctcttct ttggacagca tggccgatcc gggatggtgg tcagaatggc tcaacattcc 1560
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121 tcgggaaagg caaagaaact ggaaggcaga gtccctaacy ttgcatctta ttcggagctg 1800
123 gcagttctgt tcacgggtcca ttgccggcaa tggatgtctt tgtggtgatg atccttcaga 1860
125 aaaggatgcc tctgtttaaa aacaaattgc ttttgtgtcc ctgaagtatt taataagaag 1920
127 ctttttgcac tctagaaagt atgtttgtgt tggtttttta agaagtctaa atgaagttat 1980
129 taataacctga agctttaagt taagtgcatt gatcatatga tttttttgga agcatacaat 2040
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144 <223> OTHER INFORMATION: n is either a, c, g, or t.
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156 <223> OTHER INFORMATION: n is either a, c, g, or t.
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161 <222> LOCATION: (1348)..(1348)
162 <223> OTHER INFORMATION: n is either a, c, g, or t.

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165 <400> SEQUENCE: 2

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 168 tgtgctggaa attcggcacg aggggtgtggg gagccggggc cggcccgggg cgcgggctgg 120
 170 ggagccgggg cgagggggcg cggcccgccg ccgagatttc cccctttcta gggtaggat 180
 172 ggttctacac agccaccggg agttccctag ttgaaagggt cgccttctg tgacagaatg 240
 174 tggtaattgt aatctttaac attttcatgt aaaacatatt tcctgatcat ctttccattg 300
 176 tcttcatgga aaattgataa atatttgtgc cttccaactc tcgtcttggg tgaatgactt 360
 178 catcttaata caacatggac accacgttgc tgaaaacatg ctttgggact gccactgaat 420
 180 ttatcttttg cggttttatg acaaagttat tagtagtttc ccttttttga attagtattt 480
 182 tgaagttaat atcacaatga gttcaggctt atggagccaa gaaaaagtca cttcaccta 540
 184 ctgggaagag cggatttttt ctttgccttc tcaagaatgc agcgttacag acaaacaaac 600
 186 acaaaagctc cttaaagtac cgaagggaag tataggacag tatattcaag atcgttctgt 660
 188 ggggcattca aggattcctt ctgcaaaagg caagaaaat cagattggat taaaaattct 720
 W > 190 agagcaacct catgcagttc tctttgttga tgaaanggat gttgtagaga taaatgaaaa 780
 192 gttcacagag ttaacttttg caattaccaa ttgtgaggag aggttcagcc tgtttaaaaa 840
 194 cagaaacaga ctaagtaaag gctccaaat agacgtgggc tgtcctgtga aagtacagct 900
 196 gagatctggg gaagaaaaat ttctggagt tgtacgttc agaggacccc tgttagcaga 960
 198 gaggacagtc tccggaatat tctttggagt tgaattgctg gaagaaggtc gtggtcaagg 1020
 200 tttcactgac ggggtgtacc aagggaaca gctttttcag tgtgatgaag attgtggcgt 1080
 202 gtttgttgca ttggacaagc tagaactcat agaagatgat gacactgcat tggaaagtga 1140
 204 ttacgcaggt cctggggaca caatgcaggt cgaacttcct cctttggaaa taaactccag 1200
 206 agtttctttg aagggtggag aaacaataga atctggaaca gttatattct gtgatgtttt 1260
 OK > 208 gccaggaaaa gaaagcttag gatattttgt tgggtgtggac atggataacc ctattggcaa 1320
 210 ctgggatgga agatttgatg gagtgcanct ttgtagtttt gcgtgtgttg aaagtacaat 1380
 212 tctattgcac atcaatgata tcatccaga gagtgtgacg caggaaagga ggccctccaa 1440
 214 acttgccctt atgtcaagag gtgttgggga caaaggttca tccagtcata ataaaccaa 1500
 216 ggctacagga tctacctcag accctggaaa tagaamcaga tctgaattat tttatacctt 1560
 218 aatgggtct tctgttgact cacaaccaca atccaaatca aaaaatacat ggtacattga 1620
 220 tgaagttgca gaagaccctg caaaatctct tacagagata tctacagact ttgaccgttc 1680
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 240 aatggaaaaa gaaggcttgg agataatgat tgggaagaag aaaggcatcc aggggtcatta 2280
 242 caattcttgt tacttagact caaccttatt ctgcttattt gcttttagtt ctgttctgga 2340
 244 cactgtgtta cttagaccca aagaaaagaa cgatgtagaa tattatagt aaaccaaga 2400
 246 gctactgagg acagaaattg ttaatcctct gagaatatat ggatatgtgt gtgccacaaa 2460
 248 aattatgaaa ctgaggaaaa tacttgaaaa ggtggaggct gcatcaggat ttacctctga 2520
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 254 tatggaaaaa aatgagaaag ttggcggtcc cacaattcag cagttgttag aatggctctt 2700
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 258 atttgaaaaa gactttaaac tatttaaaaa aatttttctt tctctggaat taaatataac 2820
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264 aacctgcaac actcaagtcc accttcatcc gaagaggctg aatcataaat ataaccagct 3000
266 gtcacttccc aaagacttac ccgactggga ctggagacac ggctgcatcc cttgccagaa 3060
268 tatggagtta tttgctgttc tctgcataga aacaagccac tatgttgctt ttgtgaagta 3120
270 tgggaaggac gattctgcct ggctcttctt tgacagcatg gccgatcggg atgggtggtca 3180
272 gaatggcttc aacattcctc aagtcacccc atgccagaa gtaggagagt acttgaagat 3240
274 gtctctggaa gacctgcatt ccttggaactc caggagaatc caaggctgtg cacgaagact 3300
276 gctttgtgat gcataatatgt gcatgtacca gagtccaaca atgagtttgt acaataaact 3360
278 ggggtcatcg ggaaaggcaa agaaactgaa ggcagagtcc taacgttgca tcttattcga 3420
280 gctggcagtt ctgttcacgt ccattgccgg caatggatgt ctttgtggtg atgacccctc 3480
282 agaaaaggat gcctctgttt aaaaacaaat tgcttttgtg tccctgaagt atttaataag 3540
284 aagcattttg cactctagaa agtatgtttg tgttggtttt ttaagaagtc taaatgaagt 3600
286 tattaatacc tgaagcttta agttaagtgc attgatcata tgatattttt ggaagcatac 3660
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293 <212> TYPE: PRT
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302 Glu Glu Arg Ile Phe Tyr Leu Leu Leu Gln Glu Cys Ser Val Thr Asp
303 20 25 30
306 Lys Gln Thr Gln Lys Leu Leu Lys Val Pro Lys Gly Ser Ile Gly Gln
307 35 40 45
310 Tyr Ile Gln Asp Arg Ser Val Gly His Ser Arg Ile Pro Ser Ala Lys
311 50 55 60
314 Gly Lys Lys Asn Gln Ile Gly Leu Lys Ile Leu Glu Gln Pro His Ala
315 65 70 75 80
318 Val Leu Phe Val Asp Glu Asp Val Val Glu Ile Asn Glu Lys Phe Thr
319 85 90 95
322 Glu Leu Leu Leu Ala Ile Thr Asn Cys Glu Glu Arg Phe Ser Leu Phe
323 100 105 110
326 Lys Asn Arg Asn Arg Leu Ser Lys Gly Leu Gln Ile Asp Val Gly Cys
327 115 120 125
330 Pro Val Lys Val Gln Leu Arg Ser Gly Glu Glu Lys Phe Pro Gly Val
331 130 135 140
334 Val Arg Phe Arg Gly Pro Leu Leu Ala Glu Arg Thr Val Ser Gly Ile
335 145 150 155 160
338 Phe Phe Gly Val Glu Leu Leu Glu Glu Gly Arg Gly Gln Gly Phe Thr
339 165 170 175
342 Asp Gly Val Tyr Gln Gly Lys Gln Leu Phe Gln Cys Asp Glu Asp Cys
343 180 185 190
346 Gly Phe Val Ala Leu Asp Lys Leu Glu Leu Ile Glu Asp Asp Thr
347 195 200 205
350 Ala Leu Glu Ser Asp Tyr Ala Gly Pro Gly Asp Thr Met Gln Val Glu
351 210 215 220
354 Leu Pro Pro Leu Glu Ile Asn Ser Arg Val Ser Leu Lys Gly Gly Glu
355 225 230 235 240

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358 Thr Ile Glu Ser Gly Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys
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362 Glu Ser Leu Gly Tyr Phe Val Gly Val Asp Met Asp Asn Pro Ile Gly
363          260          265          270
366 Asn Trp Asp Gly Arg Phe Asp Gly Val Leu Cys Ser Phe Ala Cys Val
367          275          280          285
370 Glu Ser Thr Ile Leu Leu His Ile Asn Asp Ile Ile Pro Glu Ser Val
371          290          295          300
374 Thr Gln Glu Arg Arg Pro Lys Leu Ala Phe Met Ser Arg Gly Val
375 305          310          315          320
378 Gly Asp Lys Gly Ser Ser Ser His Asn Lys Pro Lys Ala Thr Gly Ser
379          325          330          335
382 Thr Ser Asp Pro Gly Asn Arg Arg Ser Glu Leu Phe Tyr Thr Leu Asn
383          340          345          350
386 Gly Ser Ser Val Asp Ser Gln Pro Gln Ser Lys Ser Lys Asn Thr Trp
387          355          360          365
390 Tyr Ile Asp Glu Val Ala Glu Asp Pro Ala Lys Ser Leu Thr Glu Ile
391          370          375          380
394 Ser Thr Asp Phe Asp Arg Ser Ser Pro Pro Leu Gln Pro Pro Pro Val
395 385          390          395          400
398 Asn Ser Leu Thr Thr Glu Asn Arg Phe His Ser Leu Pro Phe Ser Leu
399          405          410          415
402 Thr Lys Met Pro Asn Thr Asn Gly Ser Ile Gly His Ser Pro Leu Ser
403          420          425          430
406 Leu Ser Ala Gln Ser Val Met Glu Glu Leu Asn Thr Ala Pro Val Gln
407          435          440          445
410 Glu Ser Pro Pro Leu Ala Met Pro Pro Gly Asn Ser His Gly Leu Glu
411          450          455          460
414 Val Gly Ser Leu Ala Glu Val Lys Glu Asn Pro Pro Phe Tyr Gly Val
415 465          470          475          480
418 Ile Arg Trp Ile Gly Gln Pro Pro Gly Leu Asn Glu Val Leu Ala Gly
419          485          490          495
422 Leu Glu Leu Glu Asp Glu Cys Ala Gly Cys Thr Asp Gly Thr Phe Arg
423          500          505          510
426 Gly Thr Arg Tyr Phe Thr Cys Ala Leu Lys Lys Ala Leu Phe Val Lys
427          515          520          525
430 Leu Lys Ser Cys Arg Pro Asp Ser Arg Phe Ala Ser Leu Gln Pro Val
431          530          535          540
434 Ser Asn Gln Ile Glu Arg Cys Asn Ser Leu Ala Phe Gly Gly Tyr Leu
435 545          550          555          560
438 Ser Glu Val Val Glu Glu Asn Thr Pro Pro Lys Met Glu Lys Glu Gly
439          565          570          575
442 Leu Glu Ile Met Ile Gly Lys Lys Lys Gly Ile Gln Gly His Tyr Asn
443          580          585          590
446 Ser Cys Tyr Leu Asp Ser Thr Leu Phe Cys Leu Phe Ala Phe Ser Ser
447          595          600          605
450 Val Leu Asp Thr Val Leu Leu Arg Pro Lys Glu Lys Asn Asp Val Glu
451          610          615          620
454 Tyr Tyr Ser Glu Thr Gln Glu Leu Leu Arg Thr Glu Ile Val Asn Pro

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VERIFICATION SUMMARY

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L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2